Amendments to the Specification

Please amend the paragraph beginning at page 1, line 2, as follows:

--CLAIM OF PRIORITY

This application ~~claims priority under 35 USC 371 to~~ is the national stage application of International Application No. PCT/EP2005/00751, filed on January 26, 2005, which is incorporated by reference in its entirety, which claims priority to German Patent Application No. 10 2004 003 860.0, filed on January 26, 2004~~, each of which is incorporated by reference in its entirety~~.--

Please insert a new paragraph beginning at page 1, before the paragraph beginning with "The present invention relates to a method for genotyping and pathotyping bacteria species *Pseudomonas aeruginosa* by means of hybridization assays on a biochip or a microassay." as follows:

--TECHNICAL FIELD--

Please insert a new paragraph beginning at page 1, before the paragraph beginning with "*Pseudomonas aeruginosa* is an ubiquitous environmental pathogen, which, being an opportunistic pathogen, causes high morbidity and mortality in patients being locally or systemically immunocompromised." as follows:

--BACKGROUND--

Please insert a new paragraph beginning at page 2, line 21, before the paragraph beginning with "According to the present invention these problems are solved by providing a biochip or nucleic acid chip having oligonucleotide probes for specifically detecting bacterial strains of the species *Pseudomonas aeruginosa.*" as follows:

--SUMMARY--

Please insert the following paragraphs beginning at page 3, line 20, before the paragraph beginning with "For the description of the present invention, inter alia, the following definitions are used:" as follows:

--BRIEF DESCRIPTION OF THE DRAWINGS

FIGS. 1-15 show hybridized DNA chips, which were hybridized with different *P. aeruginosa* strains. Processing of the strains was performed according to the protocol described below.

FIG. 16 shows a laboratory reaction tube of typical shape and size.

FIG. 17 shows the nucleotide sequences of the primers used in the Example (SEQ ID NOS 176-207 and 209-281, respectively, in order or appearance).

FIGS. 18-21 show oligonucleotide probes according to the present invention as well as the layout of the oligonucleotide probes on the nucleic acid chip according to the present invention. Figure 18 discloses SEQ ID NOS 72-73, 76-81, 84-91 and 5-63, respectively, in order of appearance. Figure 19 discloses SEQ ID NOS 72-79, 82-109, 174-175, 171-173, 120, 152-153, 121-123, 131-132, 124-128, 37-38, 154, 133-134 and 155-158, respectively, in order of appearance.

DETAILED DESCRIPTION--

Please amend the paragraph starting on page 11, line 18 as follows:

--In particular, the oligonucleotide probes of the nucleic acid chip according to the present invention are specific for nucleic acids having a base substitution in comparison with the sequence of the reference strain of *Pseudomonas aeruginosa.* The sequence of the genome of PAO1 strain, which is accessible via [[http://]]www.pseudomonas.com, is taken as reference. Preferably, the oligonucleotide probes are specific for nucleic acids having a base substitution in comparison with the sequence of conserved genes of the reference strain PAO1 of *Pseudomonas aeruginosa.* It is further preferred that said base substitution is present in at least 20%, at least 25%, at least 30%, at least 35%, at least 40%, and particularly preferably in at least 50% of a population of *Pseudomonas aeruginosa.* This means that according to the present invention single nucleotide polymorphisms (SNPs) from conserved *Pseudomonas*

aeruginosa genes, which for example have a base substitution in at least 30% and particularly preferably in at least 50% of the population, are in particular selected for the typing. In this manner, strains of *Pseudomonas aeruginosa* can be determined or identified with a detection accuracy of more than 99.7%.--

Please amend the paragraph starting on page 20, line 17 as follows:

--The degree of sequence identity of a nucleic acid probe molecule with the oligonucleotide probe molecules explicitly referred to in the above can be determined by means of conventional algorithms. Suitable to this end is, for example, the program for determining the sequence identity, which is accessible via [[http://]]www.ncbi.nlm.gov/BLAST (on this site, for example, the link "Standard nucleotide-nucleotide BLAST [blastn]").--

Please delete the following paragraphs on page 46, line 1, as follows:

~~Figures~~

~~Figures 1 to 15 show hybridized DNA chips, which were hybridized with different *P. aeruginosa* strains. Processing of the strains was performed according to the protocol described below.~~

~~Figure 16 shows a laboratory reaction tube of typical shape and size.~~

~~Figure 17 shows the nucleotide sequences of the primers used in the Example (SEQ ID NOS 176-207 and 209-281, respectively, in order or appearance).~~

~~Oligonucleotide probes according to the present invention as well as the layout of the oligonucleotide probes on the nucleic acid chip according to the present invention are shown in Figures 18 to 21. Figure 18 discloses SEQ ID NOS 72-73, 76-81, 84-91 and 5-63, respectively, in order of appearance. Figure 19 discloses SEQ ID NOS 72-79, 82-109, 174-~~

~~175, 171-173, 120, 152-153, 121-123, 131-132, 124-128, 37-38, 154, 133-134 and 155-158, respectively, in order of appearance.~~